Abstract

Bioinformatics is concerned with creation and advancement of algorithms using techniques such as computational intelligence, applied mathematics and statistics to solve biological problems. Sequence analysis, protein structure alignment analysis and prediction, gene finding are said to be major research efforts done in the area of bioinformatics. Proteins are considered as one of the most important elements in the process of life. The activities and functions of proteins can be determined by protein sequence motifs. Identifying such motifs is one of the crucial tasks in the area of bioinformatics. In this study, Singular Value Decomposition (SVD) is adopted to select significant sequence segments and then K-Harmonic
Means granular computing model is proposed to generate protein sequence motif information efficiently. Experimental result shows that K-Harmonic granular computing model outperforms K-Means granular technique.

References

K-Harmonic Means Granular Computing Model for Protein Sequence Motif Identification


Index Terms
Computer Science
Information Technology

Keywords
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